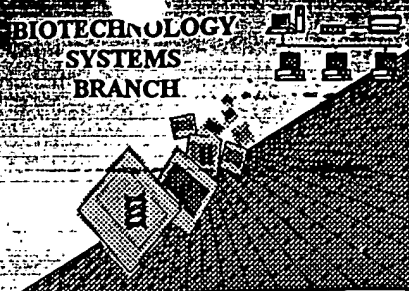


RAW SEQUENCE LISTING
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/077,574

Source: 1645

Date Processed by STIC: 8-15-00

#10

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/077,574

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1645

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/077,574

DATE: 08/15/2000
 TIME: 15:10:21

Input Set : A:\davi60seq.txt
 Output Set: N:\CRF3\08152000\I077574.raw

Does Not Comply
 Corrected Diskette Needed

See pp. 1, 5

3 <110> APPLICANT: PANACCIO, Michael
 4 HASSE, Detlef
 6 <120> TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC COMPOSITIONS
 8 <130> FILE REFERENCE: p:\oper\mro\08-077574
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/077,574
 11 <141> CURRENT FILING DATE: 1998-09-24
 13 <150> PRIOR APPLICATION NUMBER: AU PN 6910
 14 <151> PRIOR FILING DATE: 1995-11-30
 16 <150> PRIOR APPLICATION NUMBER: AU PN 6911
 17 <151> PRIOR FILING DATE: 1995-11-30
 19 <150> PRIOR APPLICATION NUMBER: PCT/AU/00767
 20 <151> PRIOR FILING DATE: 1996-11-29
 22 <160> NUMBER OF SEQ ID NOS: 34
 24 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

885 <210> SEQ ID NO: 14
 886 <211> LENGTH: 86
 887 <212> TYPE: PRT
 888 <213> ORGANISM: Lawsonia intracellularis
 890 <400> SEQUENCE: 14
 891 Ile Pro Leu His Val Gly Tyr Gly Thr Phe Ser Pro Val Leu Cys Asn
 892 1 10 15
 W--> 894 Asp Ile Pro Lys His Leu Ile Xaa Ser Glu Phe Val His Phe Pro Glu
 895 20 25 30
 W--> 897 Thr Xaa Phe Ser Thr Ile Leu Asn Ala Arg Phe Ala Xaa Glu Tyr Leu
 898 35 40 45
 E--> 900 ys Ser Ala Ile Gly Asp Pro Leu Leu Ser Pro Pro Leu Xaa Gly Cys
 901 50 55 60
 903 Tyr Leu Thr Pro Phe Ala Arg Gly Ser Pro Pro Gln Pro Tyr Ser Ile
 904 65 70 75 80
 W--> 906 Xaa Phe Ser Ser Gln Ile
 907 85

Missing mandatory <220> to
 <223> features to explain
 "Xaa's" in sequence.

See #10 on
 Error Summary

Sheet. This error
 has been indicated
 in other sequences.
 Please check entire
 listing and correct.

invalid amino acid designator.

RECEIVED

AUG 21 2000

TECH CENTER 1600/2900

VERIFICATION SUMMARY

DATE: 08/15/2000

PATENT APPLICATION: US/09/077,574

TIME: 15:10:22

Input Set : A:\davia60seq.txt

Output Set: N:\CRF3\08152000\I077574.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:90 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:94 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:122 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:523 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:523 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:523 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:523 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:523 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:525 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:525 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:525 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:525 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:527 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:527 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:527 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:527 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:550 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:550 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:551 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:554 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:555 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:590 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:590 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:590 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:590 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:590 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:600 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8

VERIFICATION SUMMARY

DATE: 08/15/2000

PATENT APPLICATION: US/09/077,574

TIME: 15:10:22

Input Set : A:\davie60seq.txt

Output Set: N:\CRF3\08152000\I077574.raw

L:600 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
 L:600 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
 L:600 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
 L:600 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
 L:670 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
 L:670 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
 L:687 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
 M:340 Repeated in SeqNo=9
 L:698 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:702 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:706 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:710 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:714 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:718 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:722 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:724 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
 L:725 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
 L:726 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:759 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
 L:759 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
 L:759 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
 L:759 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
 L:759 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
 L:790 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
 L:790 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
 L:790 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
 L:790 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
 L:790 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
 L:808 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 L:808 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
 L:809 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 M:340 Repeated in SeqNo=12
 L:820 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 L:821 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 L:824 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 L:825 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 L:828 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 L:829 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 L:836 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 L:837 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 L:840 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 L:841 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 L:844 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 L:845 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
 L:864 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
 M:340 Repeated in SeqNo=13
 L:894 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
 M:340 Repeated in SeqNo=14
 L:900 M:333 E: Wrong sequence grouping, Amino acids not in groups!

VERIFICATION SUMMARY

DATE: 08/15/2000

PATENT APPLICATION: US/09/077,574

TIME: 15:10:22

Input Set : A:\davie60seq.txt

Output Set: N:\CRF3\08152000\I077574.raw

L:900 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:936 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
M:340 Repeated in SeqNo=15
L:988 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
M:340 Repeated in SeqNo=17
L:1197 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
M:340 Repeated in SeqNo=28
L:1234 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:29
M:340 Repeated in SeqNo=29
L:1271 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:30
M:340 Repeated in SeqNo=30
L:1316 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:31
M:340 Repeated in SeqNo=31
L:1337 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
M:340 Repeated in SeqNo=32
L:1368 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:33
M:340 Repeated in SeqNo=33
L:1385 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
M:340 Repeated in SeqNo=34

09/077, 574

p.5 Sequence # 5 (last three lines)

yattgsatwa gaaacttttg rggtrrrcta tgaacaaaca acca(n)caac ggcca(n)ac 4860

at(n)ncag(n)t tggggtcata ggggccacgc tttatgtacg tacaaccc(n) actgaaattc 4920

tgg(n)ttg(n)tt tggggg(n)naa (n)tggggtatcg caa(n)c(n)t(n)c cccccccct gg 4972

Missing mandatory <220> to <223> features to explain "n's" in sequence. See #10 on Error Summary Sheet. *Please check entire sequence listing for this same error.*

"n's" and "Xaa's" in sequences must have mandatory <220> to <223> features.

<220> Leave blank

<221> Name/Key

<222> Location

<223> Other Information

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

F.Y.I.